Abstract

Understanding of carbon cycling in coniferous forests that represent a large carbon sink is crucial for our understanding of natural processes under global climate change. Recognition of fungi as fundamental decomposers can contribute to this understanding. Fungi are able to decompose numbers of substrates and possess a variety of enzymes to do so

In this study I present litter decomposing fungi in mountain spruce forest from national park Šumava. The aim of my thesis was to follow succession and community changes of fungi from the early stages of decomposition of *Picea abies* needles until degradation of organic matter in the organic horizon of the soil. This aim was accomplished partly by recording the extracellular enzyme production of fungi in different stages of decomposition from needles attached to the twigs of a fallen tree to a litter material in later stages of decomposition on the soil surface. In addition to testing of fungi on their natural substrata – needle litter, enzyme activities were also measured in laboratory agar cultures, which allow comparison of diverse fungi with different origins. Enzyme activities were aimed at enzymes decomposing cellulose and compounds found in litter. Although ecology of endophytic and saprothrophic fungi suggest differences in enzyme production, these were not recorded. Enzyme activity peaks as poor malt extract agar becomes spent and the only nutritive source – spruce needles is difficult to decompose.

Another part of research was triggered on fungal communities isolated from the soil where decomposition of needles continues. Fungal communities in the soil were approached by 454–pyrosequencing method of the whole meatgenome. The focus of 454–pyrosequencing study was on a total and cellulolytic fungal community represented by *cbhI* gene as a proxy. To characterize *cbhI* gene in detail, its sequences from some of the fungi isolated from spruce needles were cloned. I have investigated to what extent does the abundance of fungi in general and cellulolytic fungi in particular, differ among soil horizons and seasons. I have confirmed that horizon strongly discriminates between fungal ecological groups. Saprotrophic fungi were found in L horizon while most of mycorhizzal in H horizon. The abundance of *Basidiomycota* in the organic horizon was higher than of *Ascomycota* and vice versa. I have found significant association with one of soil horizons for 73% of examined part of total fungal community and with a season for 37%. In examined part of community represented by *cbhI* gene pool, 62% OTUs depend on a soil horizon and 21% on a specific

season. The results show, that fungal communities are strongly influenceable by environmental factors.

Keywords (12): Fungal community**,** *Picea abies*, 454–pyrosequencing, *cbhI* – cellobiohydrolase I, ITS – internal transcribed spacer, Cellulose, Litter horizon, Organic/organic horizon, Enzymes, Saprotrophic, mycorrhizal and parasitic fungi, Forest soil